

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising:
  - (a) a first nucleotide sequence encoding a first polypeptide comprising at least 200 amino acids, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 70% identity based on the Clustal alignment method,
  - (b) a second nucleotide sequence encoding a second polypeptide comprising at least 200 amino acids, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 85% identity based on the Clustal alignment method,
  - (c) a third nucleotide sequence encoding a third polypeptide comprising at least 300 amino acids, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:18 have at least 70% identity based on the Clustal alignment method, or
  - (d) the complement of the first, second, or third nucleotide sequence, wherein the complement and the first, second, or third nucleotide sequence contain the same number of nucleotides and are 100% complementary.
2. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 80% identity based on the Clustal alignment method, and wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:18 have at least 80% identity based on the Clustal alignment method.
3. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 85% identity based on the Clustal alignment method, and wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:18 have at least 85% identity based on the Clustal alignment method.
4. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 90% identity based on the Clustal alignment method, and wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:18 have at least 90% identity based on the Clustal alignment method.
5. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least

95% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 95% identity based on the Clustal alignment method, and wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:18 have at least 95% identity based on the Clustal alignment method.

6. The isolated polynucleotide of Claim 1, wherein the first polypeptide comprises the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10, wherein the second polypeptide comprises the amino acid sequence of SEQ ID NO:14, and wherein the third polypeptide comprises the amino acid sequence of SEQ ID NO:18.

7. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:3 or SEQ ID NO:9, wherein the second nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:13, and wherein the third nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:17.

8. The isolated polynucleotide of Claim 1, wherein the first, second, and third polypeptides are brittle-1 homologs.

9. A chimeric gene comprising the polynucleotide of Claim 1 operably linked to a regulatory sequence.

10. A vector comprising the polynucleotide of Claim 1.

11. An isolated polynucleotide fragment comprising a nucleotide sequence comprised by the polynucleotide of Claim 1, wherein the nucleotide sequence contains at least 30 nucleotides.

12. The fragment of Claim 11, wherein the nucleotide sequence contains at least 40 nucleotides.

13. The fragment of Claim 11, wherein the nucleotide sequence contains at least 60 nucleotides.

14. An isolated polypeptide comprising:

(a) a first amino acid sequence comprising at least 200 amino acids, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 70% identity based on the Clustal alignment method,

(b) a second amino acid sequence comprising at least 200 amino acids, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 85% identity based on the Clustal alignment method, or

(c) a third amino acid sequence comprising at least 300 amino acids, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:18 have at least 70% identity based on the Clustal alignment method.

15. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 80% identity based on the Clustal alignment method, and wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:18 have at least 80% identity based on the Clustal alignment method.
16. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 85% identity based on the Clustal alignment method, and wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:18 have at least 85% identity based on the Clustal alignment method.
17. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 90% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 90% identity based on the Clustal alignment method, and wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:18 have at least 90% identity based on the Clustal alignment method.
18. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10 have at least 95% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 95% identity based on the Clustal alignment method, and wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:18 have at least 95% identity based on the Clustal alignment method.
19. The polypeptide of Claim 14, wherein the first amino acid sequence comprises the amino acid sequence of SEQ ID NO:4 or SEQ ID NO:10, wherein the second amino acid sequence comprises the amino acid sequence of SEQ ID NO:14, and wherein the third amino acid sequence comprises the amino acid sequence of SEQ ID NO:18.
20. The polypeptide of Claim 14, wherein the polypeptide is a brittle-1 homolog.
21. A method for transforming a cell comprising introducing the polynucleotide of Claim 1 into a cell.
22. A cell comprising the chimeric gene of Claim 9.
23. A method for producing a transgenic plant comprising transforming a plant cell with the polynucleotide of Claim 1 and regenerating a plant from the transformed plant cell.
24. A plant comprising the chimeric gene of Claim 9.
25. A seed comprising the chimeric gene of Claim 9.